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AMENDMENT
Docket No. GP091-02.UT

Amendments to the claims:

Please amend Claims 1, 2, 3, 15, 16, and 17 as shown below.

1. (Currently amended) A method for detecting a fusion nucleic acid comprising the steps of:

a) providing a sample containing a first single-stranded fusion nucleic acid comprising a *bcr-abl* splice junction site;

b) contacting under nucleic acid amplification conditions:

the first single-stranded fusion nucleic acid,

a first primer which hybridizes to the fusion nucleic acid at a first primer binding site of SEQ ID NO:22 located 3' to the splice junction site, and

at least one enzyme having nucleic acid polymerase activity;

c) amplifying the fusion nucleic acid in a single isothermal nucleic acid amplification reaction using the first primer to produce a plurality of second nucleic acid strands complementary to at least a portion of the first single-stranded fusion nucleic acid that contains the *bcr-abl* splice junction site, wherein each second nucleic acid strand comprises:

a complementary splice junction site,

a first probe binding site located 3' to and not overlapping the complementary splice junction site, and

a second probe binding site located 5' to and not overlapping the complementary splice junction site;

d) hybridizing the second nucleic acid strands with an oligonucleotide probe under hybridization conditions in which the probe hybridizes to the first or second probe binding site, thereby forming a probe:target hybrid; and

e) detecting the probe:target hybrid as an indication of the presence of the fusion nucleic acid in the sample.

2. (Currently amended) The method of Claim 1, wherein the first single-stranded fusion nucleic acid is an mRNA, the first primer is a promoter-primer, the enzyme having nucleic acid polymerase activity comprises an RNA polymerase activity, and the oligonucleotide probe is of the same sense as the mRNA and binds to the first probe binding site.

3. (Currently amended) The method of Claim 1, wherein the first single-stranded fusion nucleic acid is a mRNA, wherein the second nucleic acid strands are complementary RNA, wherein the amplifying step includes contacting the second nucleic acid strand with a second primer or promoter-primer which hybridizes to a second primer binding site that hybridizes to SEQ ID NO:5 located 3' to both the complementary splice junction site and the first probe binding site, and wherein the amplifying step uses an enzyme having nucleic acid polymerase activity comprising an RNA polymerase activity, and an enzyme having nucleic acid polymerase activity comprising a DNA-directed DNA polymerase activity and an RNA-directed DNA polymerase activity.

4. (Canceled previously)

5. (Previously amended) The method of Claim 1, wherein the oligonucleotide probe has a sequence of SEQ ID NO:9 or SEQ ID NO:27.

6. (Previously amended) The method of Claim 1, wherein step a) includes preparing RNA from the sample containing the fusion nucleic acid by:

contacting a biological sample comprising the fusion nucleic acid with a solution consisting essentially of:

a buffer,

about 150 mM to about 1 M of a soluble salt,

about 0.5% to about 1.5% (v/v) of a non-ionic detergent, and

a solid support to which is joined an immobilized oligonucleotide comprising a nucleotide base sequence which forms, directly or indirectly, a stable hybridization complex with an RNA under conditions permitting the formation of the stable hybridization complex; and

separating the hybridization complex joined to the solid support from unhybridized sample components without extracting the RNA using reagents such as phenol or chloroform.

7. (Original) The method of Claim 6, wherein the fusion nucleic acid is mRNA.

8. (Original) The method of Claim 7, wherein the nucleotide base sequence of the immobilized oligonucleotide comprises a poly-T sequence.

9. (Previously amended) A method of detecting a fusion mRNA transcript produced as a result of a chromosomal translocation comprising the steps of:

a) providing a sample containing a fusion mRNA transcript comprising a *bcr-abl* splice junction site;

b) contacting under isothermal nucleic acid amplification conditions:

the fusion mRNA transcript,

a first primer which hybridizes to a sequence of SEQ ID NO:22, and

at least one enzyme having nucleic acid polymerase activity;

c) amplifying the fusion mRNA transcript in a single nucleic acid amplification reaction that uses

the first primer to produce a plurality of second nucleic acid strands complementary to at least a portion of the fusion mRNA transcript containing the splice junction site, wherein each second nucleic acid strand comprises:

a complementary splice junction site,

a first probe binding site located 3' to and not overlapping the complementary splice junction site, and

a second probe binding site located 5' to and not overlapping the complementary splice junction site, wherein the second probe binding site overlaps or is located 3' to sequence complementary to SEQ ID NO:22;

d) hybridizing the second nucleic acid strands with an oligonucleotide probe which hybridizes to the second nucleic acid strands at either the first probe binding site or the second probe binding site but does not hybridize to the fusion mRNA transcript, thereby forming a hybridization complex of the first probe or the second probe and the second nucleic acid strand; and

e) detecting the hybridization complex as an indication of the presence of the fusion transcript in the sample.

10. (Previously amended) The method of Claim 9, wherein the amplifying step uses only a first primer that is a promoter primer of SEQ ID NO:1 and the enzyme has an RNA polymerase activity, and wherein the hybridizing step uses an oligonucleotide probe which hybridizes to the second nucleic acid at the first probe binding site.

11. (Previously canceled)

12. (Original) The method of Claim 9, wherein the first probe binding site is derived from a different

chromosome than the chromosome from which the second probe binding site is derived, and the fusion mRNA transcript detected results from a translocation involving different chromosomes.

13. (Previously canceled)

14. (Previously amended) The method of Claim 9, wherein the fusion mRNA transcript results from a human t(9;22) translocation.

15. (Currently amended) One or more oligonucleotides suitable for use in the method of Claim 14, wherein a nucleotide sequence of the one or more oligonucleotides is ~~have a sequence~~ selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, ~~to~~ SEQ ID NO:23, SEQ ID NO:26 and SEQ ID NO:27.

16. (Currently amended) The method of Claim 9, wherein the amplifying step uses an enzyme having nucleic acid polymerase activity comprising an RNA polymerase activity, and an enzyme having nucleic acid polymerase activity comprising a DNA-directed DNA polymerase activity, and an RNA-directed DNA polymerase activity, and further uses a second primer or promoter primer which hybridizes under amplification conditions to a nucleotide sequence of a complementary RNA produced during the amplifying step.

17. (Currently amended) The method of Claim 16, wherein the enzyme having nucleic acid polymerase activity comprising RNA-directed DNA polymerase activity and DNA-directed DNA

polymerase activity ~~are supplied by~~ is a reverse transcriptase.

18. (Previously amended) The method of Claim 9, wherein the amplifying step also amplifies an internal control normal *abl* transcript in the sample by using the first primer to amplify a normal *abl* sequence in SEQ ID NO:25 and then hybridizing an oligonucleotide probe which hybridizes to the complement of the internal control transcript but does not hybridize to the complement of the fusion mRNA transcript thereby forming in internal control hybridization complex, and wherein the detecting step also detects the presence of the internal control hybridization complex in the sample, thereby providing an internal standard.

19. (Previously canceled)

20. (Previously amended) The method of Claim 6, wherein the biological sample is uncoagulated blood, plasma or bone marrow.

21. (Previously amended) A method of detecting a fusion mRNA transcript produced as a result of a human *bcr-abl* translocation comprising the steps of:

a) providing a sample containing a human fusion mRNA transcript comprising a *bcr-abl* splice junction site;

b) contacting under isothermal nucleic acid amplification conditions:

the fusion mRNA transcript,

a first primer that binds to a primer binding site of SEQ ID NO:22, which is located in an *abl* sequence flanking the *bcr-abl* splice junction site,

a second primer having a sequence of SEQ ID NO:5, which hybridizes to a *bcr*

sequence flanking the *bcr-abl* splice junction site,

at least one enzyme having an RNA-directed DNA polymerase activity, and

at least one enzyme having an DNA-directed RNA polymerase activity;

c) amplifying the fusion mRNA transcript in a single nucleic acid amplification reaction that uses

the first primer,

the second primer, and

the DNA-dependent RNA polymerase activity to produce amplified RNA that is complementary to the fusion mRNA transcript comprising the *bcr-abl* splice junction;

d) hybridizing the amplified RNA with an oligonucleotide probe which hybridizes to a probe binding site located in an amplified *bcr* sequence flanking the *bcr-abl* splice junction, thereby forming a hybridization complex; and

e) detecting the hybridization complex as an indication of the presence of the fusion mRNA transcript in the sample.

22. (Previously amended) The method of claim 21, further comprising:

in the contacting step, contacting a third primer having a sequence of SEQ ID NO:13 that hybridizes to the complement of a normal *abl* mRNA transcript,

in the amplifying step, amplifying a normal *abl* sequence present in the normal *abl* mRNA by using the first primer and the third primer,

in the hybridizing step, hybridizing an oligonucleotide probe that hybridizes to a probe binding site located in an amplified normal *abl* sequence that is missing in amplified RNA made from the fusion mRNA transcript, and

in the detecting step, detecting a hybridization complex made up of the probe hybridized to the amplified normal *abl* sequence that is missing in amplified RNA made from the fusion mRNA transcript.

thereby providing an internal control based on amplifying and detecting normal *abl* sequence.

23. (Previously amended) The method of claim 21, wherein the first primer is of SEQ ID NO:1, the second primer is of SEQ ID NO:5, and the probe is of SEQ ID NO:9 or SEQ ID NO:27 or is a mixture of SEQ ID NO:9 and SEQ ID NO:27.

24. (Previously added) The method of claim 21, wherein the first primer is of SEQ ID NO:1, the second primer is of SEQ ID NO:5 or its RNA equivalent, and the probe is of SEQ ID NO:9 or its RNA equivalent.

25. (Previously added) The method of claim 21, wherein the first primer is of SEQ ID NO:1, the second primer is of SEQ ID NO:5, and the probe is of SEQ ID NO:27.

26. (Previously amended) The method of claim 22, wherein the third primer is of SEQ ID NO:13 or its RNA equivalent, and the oligonucleotide probe that hybridizes to the amplified normal *abl* sequence is of SEQ ID NO:16 or its RNA equivalent or SEQ ID NO:26.

27. (Previously added) The method of claim 9, wherein the first primer is of SEQ ID NO:1, the first probe is of SEQ ID NO:9, and the second probe is of SEQ ID NO:16.